AMENDMENT

<u>AMENDMENTS TO THE SPECIFICATION:</u>

Please delete the Sequence Listing and insert therefor the substitute Sequence Listing submitted as text concurrently herewith through EFS-Web.

At page 20, lines 17 through 25, please replace the paragraph with the following paragraph:

Another preferred pH-dependent membrane-binding internalizing peptide in this regard is aa1-aa2-aa3-EAALA(EALA)4-EALEALAA-amide (SEQ ID NO:601), which represents a modification of the peptide sequence of Subbarao et al. (1987). Within this peptide sequence, the first amino acid residue (aa1) is preferably a unique residue, such as C or K, that facilitates chemical conjugation of the internalizing peptide to a targeting protein conjugate. Amino acid residues 2-3 may be selected to modulate the affinity of the internalizing peptide for different membranes. For instance, if both residues 2 and 3 are K or R, the internalizing peptide will have the capacity to bind to membranes or patches of lipids having a negative surface charge. If residues 2-3 are neutral amino acids, the internalizing peptide will insert into neutral membranes.

At page 35 through page 48, please replace Table 3 with the following Table 3:

Table 3
PDZ Domains Used in Screening Assays

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
26s subunit p27	9184389	1	RDMAEAHKEAMSRKLGQSESQGPPRAFAKVNSISPGSPSI AGLQVDDEIVEFGSVNTQNFQSLHNIGSVVQHSEGALAPT ILLSVSM	191
AF6	430993	1	LRKEPEIITVTLKKQNGMGLSIVAAKGAGQDKLGIYVKSV VKGGAADVDGRLAAGDQLLSVDGRSLVGLSQERAAELM TRTSSVVTLEVAKQG	192
AIPC	12751451	1	LIRPSVISIIGLYKEKGKGLGFSIAGGRDCIRGQMGIFVKTI FPNGSAAEDGRLKEGDEILDVNGIPIKGLTFQEAIHTFKQI RSGLFVLTVRTKLVSPSLTNSS	193
AIPC	12751451	2	GISSLGRKTPGPKDRIVMEVTLNKEPRVGLGIGACCLALE NSPPGIYIHSLAPGSVAKMESNLSRGDQILEVNSVNVRHA ALSKVHAILSKCPPGPVRLVIGRHPNPKVSEQEMDEVIAR	194

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			STYQESKEANSS	
AIPC	12751451	3	QSENEEDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHR VFSQGAASQEGTMNRGDFLLSVNGASLAGLAHGNVLKV LHQAQLHKDALVVIKKGMDQPRPSNSS	195
AIPC	12751451	4	LGRSVAVHDALCVEVLKTSAGLGLSLDGGKSSVTGDGPL VIKRVYKGGAAEQAGIIEAGDEILAINGKPLVGLMHFDA WNIMKSVPEGPVQLLIRKHRNSS	196
alpha actinin-2 associated LIM protein	2773059	1	REEGGMPQTVILPGPAAWGFRLSGGIDFNQPLVITRITPGS KAAAANLCPGDVILAIDGFGTESMTHADGQDRIKAAAHQ LCLKIDRGETHLWSPHSIV	197
APXL-1	13651263	1	ILVEVQLSGGAPWGFTLKGGREHGEPLVITKIEEGSKAAA VDKLLAGDEIVGINDIGLSGFRQEAICLVKGSHKTLKLVV KRNSS	198
Atrophin-1 Interacting Protein	2947231	1	REKPLFTRDASQLKGTFLSTTLKKSNMGFGFTIIGGDEPDE FLQVKSVIPDGPAAQDGKMETGDVIVYINEVCVLGHTHA DVVKLFQSVPIGQSVNLVLCRGYP	199
Atrophin-1 Interacting Protein	2947231	2	LSGATQAELMTLTIVKGAQGFGFTIADSPTGQRVKQILDI QGCPGLCEGDLIVEINQQNVQNLSHTEVVDILKDCPIGSET SLIIHRGGFF	200
Atrophin-1 Interacting Protein	2947231	3	HYKELDVHLRRMESGFGFRILGGDEPGQPILIGAVIAMGS ADRDGRLHPGDELVYVDGIPVAGKTHRYVIDLMHHAAR NGQVNLTVRRKVLCG	201
Atrophin-1 Interacting Protein	2947231	4	EGRGISSHSLQTSDAVIHRKENEGFGFVIISSLNRPESGSTIT VPHKIGRIIDGSPADRCAKLKVGDRILAVNGQSIINMPHA DIVKLIKDAGLSVTLRIIPQEEL	202
Atrophin-1 Interacting Protein	2947231	5	LSDYRQPQDFDYFTVDMEKGAKGFGFSIRGGREYKMDL YVLRLAEDGPAIRNGRMRVGDQIIEINGESTRDMTHARAI ELIKSGGRRVRLLLKRGTGQ	203
Atrophin-1 Interacting Protein	2947231	6	HESVIGRNPEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVIKHCKDPLR LKCVKQGGIHR	204
CARD11	12382772	1	SVGHVRGPGPSVQHTTLNGDSLTSQLTLLGGNARGSFVH SVKPGSLAEKAGLREGHQLLLLEGCIRGERQSVPLDTCTK EEAHWTIQRCSGPVTLHYKVNHEGYRK	205
CARD14	13129123	1	RRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVT PGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEE AVGLLRRVDGFCCLSVKVNTDGYKR (SEQ ID NO:115)	206
CASK	3087815	1	TRVRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMI HRQGTLHVGDEIREINGISVANQTVEQLQKMLREMRGSIT FKIVPSYRTQS	207
Connector Enhancer	3930780	1	LEQKAVLEQVQLDSPLGLEIHTTSNCQHFVSQVDTQVPTD SRLQIQPGDEVVQINEQVVVGWPRKNMVRELLREPAGLS LVLKKIPIP	208
Cytohesin Binding Protein	3192908	1	QRKLVTVEKQDNETFGFEIQSYRPQNQNACSSEMFTLICK IQEDSPAHCAGLQAGDVLANINGVSTEGFTYKQVVDLIRS SGNLLTIETLNG	209

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
Densin 180	16755892	1	RCLIQTKGQRSMDGYPEQFCVRIEKNPGLGFSISGGISGQG NPFKPSDKGIFVTRVQPDGPASNLLQPGDKILQANGHSFV HMEHEKAVLLLKSFQNTVDLVIQRELTV	210
DLG1	475816	1	IQVNGTDADYEYEEITLERGNSGLGFSIAGGTDNPHIGDD SSIFITKIITGGAAAQDGRLRVNDCILQVNEVDVRDVTHSK AVEALKEAGSIVRLYVKRRN	211
DLG1	475816	2	IQLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAH KDGKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFVY LKVAKPTSMYMNDGN	212
DLG1	475816	3	ILHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKG DRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPE EYSR	213
DLG2	12736552	1	ISYVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNPHIGDDP GIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKA VEALKEAGSIVRLYVRRR	214
DLG2	12736552	2	IPILETVVEIKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTK IIDGGAAQKDGRLQVGDRLLMVNNYSLEEVTHEEAVAIL KNTSEVVYLKVGKPTTIVMTDPYGPPNSS	215
DLG2	12736552	3	ILEGEPRKVVLHKGSTGLGFNIVGGEDGEGIFVSFILAGGP ADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQT VTIIAQHQPEDYARFEAKIHDLNSS	216
DLG5	3650451	1	GIPYVEEPRHVKVQKGSEPLGISIVSGEKGGIYVSKVTVGS IAHQAGLEYGDQLLEFNGINLRSATEQQARLIIGQQCDTIT ILAQYNPHVHQLRNSSZLTD	217
DLG5	3650451	2	GILAGDANKKTLEPRVVFIKKSQLELGVHLCGGNLHGVF VAEVEDDSPAKGPDGLVPGDLILEYGSLDVRNKTVEEVY VEMLKPRDGVRLKVQYRPEEFIVTD	218
DLG6, splice variant 1	14647140	1	PTSPEIQELRQMLQAPHFKALLSAHDTIAQKDFEPLLPPLP DNIPESEEAMRIVCLVKNQQPLGATIKRHEMTGDILVARII HGGLAERSGLLYAGDKLVEVNGVSVEGLDPEQVIHILAM SRGTIMFKVVPVSDPPVNSS	219
DLG6, splice variant 2	AB05330 3	1	PTSPEIQELRQMLQAPHFKGATIKRHEMTGDILVARIIHGG LAERSGLLYAGDKLVEVNGVSVEGLDPEQVIHILAMSRG TIMFKVVPVSDPPVNSS	220
DVL1	2291005	1	LNIVTVTLNMERHHFLGISIVGQSNDRGDGGIYIGSIMKG GAVAADGRIEPGDMLLQVNDVNFENMSNDDAVRVLREI VSQTGPISLTVAKCW	221
DVL2	2291007	1	LNIITVTLNMEKYNFLGISIVGQSNERGDGGIYIGSIMKGG AVAADGRIEPGDMLLQVNDMNFENMSNDDAVRVLRDIV HKPGPIVLTVAKCWDPSPQNS	222
DVL3	6806886	1	IITVTLNMEKYNFLGISIVGQSNERGDGGIYIGSIMKGGAV AADGRIEPGDMLLQVNEINFENMSNDDAVRVLREIVHKP GPITLTVAKCWDPSP	223
ELFIN 1	2957144	1	LTTQQIDLQGPGPWGFRLVGRKDFEQPLAISRVTPGSKAA LANLCIGDVITAIDGENTSNMTHLEAQNRIKGCTDNLTLT VARSEHKVWSPLVTNSS	224
ENIGMA	561636	1	IFMDSFKVVLEGPAPWGFRLQGGKDFNVPLSISRLTPGGK AAQAGVAVGDWVLSIDGENAGSLTHIEAQNKIRACGERL	225

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			SLGLSRAQPV	
ERBIN	8923908	1	QGHELAKQEIRVRVEKDPELGFSISGGVGGRGNPFRPDDD GIFVTRVQPEGPASKLLQPGDKIIQANGYSFINIEHGQAVS LLKTFQNTVELIIVREVSS	226
EZRIN Binding Protein 50	3220018	1	QMSADAAAGAPLPRLCCLEKGPNGYGFHLHGEKGKLGQ YIRLVEPGSPAEKAGLLAGDRLVEVNGENVEKETHQQVV SRIRAALNAVRLLVVDPETDEQLQKLGVQVREELLRAQE APGQAEPPAAAEVQGAGNENEPREADKSHPEQRELRNSS	227
EZRIN Binding Protein 50	3220018	2	IQQRELRPRLCTMKKGPSGYGFNLHSDKSKPGQFIRSVDP DSPAEASGLRAQDRIVEVNGVCMEGKQHGDVVSAIRAG GDETKLLVVDRETDEFFKNSS	228
FLJ00011	10440352	1	KNPSGELKTVTLSKMKQSLGISISGGIESKVQPMVKIEKIF PGGAAFLSGALQAGFELVAVDGENLEQVTHQRAVDTIRR AYRNKAREPMELVVRVPGPSPRPSPSD	229
FLJ11215	11436365	1	EGHSHPRVVELPKTEEGLGFNIMGGKEQNSPIYISRIIPGGI ADRHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAQG KVKLVVRYTPKVLEEME	230
FLJ12428	BC012040	1	PGAPYARKTFTIVGDAVGWGFVVRGSKPCHIQAVDPSGP AAAAGMKVCQFVVSVNGLNVLHVDYRTVSNLILTGPRTI VMEVMEELEC	231
FLJ12615	10434209	1	GQYGGETVKIVRIEKARDIPLGATVRNEMDSVIISRIVKGG AAEKSGLLHEGDEVLEINGIEIRGKDVNEVFDLLSDMHGT LTFVLIPSQQIKPPPA	232
FLJ20075	7019938	1	ILAHVKGIEKEVNVYKSEDSLGLTITDNGVGYAFIKRIKD GGVIDSVKTICVGDHIESINGENIVGWRHYDVAKKLKELK KEELFTMKLIEPKKAFEI	233
FLJ21687	10437836	1	KPSQASGHFSVELVRGYAGFGLTLGGGRDVAGDTPLAVR GLLKDGPAQRCGRLEVGDLVLHINGESTQGLTHAQAVER IRAGGPQLHLVIRRPLETHPGKPRGV	234
FLJ31349	AK055911	1	PVMSQCACLEEVHLPNIKPGEGLGMYIKSTYDGLHVITGT TENSPADRSQKIHAGDEVIQVNQQTVVGWQLKNLVKKL RENPTGVVLLLKKRPTGSFNFTPEFIVTD	235
FLJ32798	AK057360	1	LDDEEDSVKIIRLVKNREPLGATIKKDEQTGAIIVARIMRG GAADRSGLIHVGDELREVNGIPVEDKRPEEIIQILAQSQGA ITFKIIPGSKEETPSNSS	236
GoRASP1	NM031899	1	MGLGVSAEQPAGGAEGFHLHGVQENSPAQQAGLEPYFD FIITIGHSRLNKENDTLKALLKANVEKPVKLEVFNMKTMR VREVEVVPSNMWGGQGLLGASVRFCSFRRASE	237
GoRASP1	NM031899	2	RASEQVWHVLDVEPSSPAALAGLRPYTDYVVGSDQILQE SEDFFTLIESHEGKPLKLMVYNSKSDSCREVTVTPNAAW GGEGSLGCGIGYGYLHRIPTQ	238
GoRASP2	13994253	1	MGSSQSVEIPGGGTEGYHVLRVQENSPGHRAGLEPFFDFI VSINGSRLNKDNDTLKDLLKANVEKPVKMLIYSSKTLELR ETSVTPSNLWGGQGLLGVSIRFCSFDGANE	239
GoRASP2	13994253	2	NENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNESE DLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGE GSLGCGIGYGYLHRIPTR	240

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
GRIP 1	4539083	1	VVELMKKEGTTLGLTVSGGIDKDGKPRVSNLRQGGIAAR SDQLDVGDYIKAVNGINLAKFRHDEIISLLKNVGERVVLE VEYE	241
GRIP 1	4539083	2	RSSVIFRTVEVTLHKEGNTFGFVIRGGAHDDRNKSRPVVI TCVRPGGPADREGTIKPGDRLLSVDGIRLLGTTHAEAMSI LKQCGQEAALLIEYDVSVMDSVATASGNSS	242
GRIP 1	4539083	3	HVATASGPLLVEVAKTPGASLGVALTTSMCCNKQVIVID KIKSASIADRCGALHVGDHILSIDGTSMEYCTLAEATQFL ANTTDQVKLEILPHHQTRLALKGPNSS	243
GRIP 1	4539083	4	HVATASGPLLVEVAKTPGASLGVALTTSMCCNKQVIVID KIKSASIADRCGALHVGDHILSIDGTSMEYCTLAEATQFL ANTTDQVKLEILPHHQTRLALKGPNSS	244
GRIP 1	4539083	5	AESVIPSSGTFHVKLPKKHNVELGITISSPSSRKPGDPLVIS DIKKGSVAHRTGTLELGDKLLAIDNIRLDNCSMEDAVQIL QQCEDLVKLKIRKDEDNSD	245
GRIP 1	4539083	6	IYTVELKRYGGPLGITISGTEEPFDPIISSLTKGGLAERTGA IHIGDRILAINSSSLKGKPLSEAIHLLQMAGETVTLKIKKQT DAQSA	246
GRIP 1	4539083	7	IMSPTPVELHKVTLYKDSDMEDFGFSVADGLLEKGVYVK NIRPAGPGDLGGLKPYDRLLQVNHVRTRDFDCCLVVPLI AESGNKLDLVISRNPLA	247
GTPase Activating Enzyme	2389008	1	LSRGCETRELALPRDGQGRLGFEVDAEGFVTHVERFTFAE TAGLRPGARLLRVCGQTLPSLRPEAAAQLLRSAPKVCVT VLPPDESGRPRNSS	248
Guanine Exchange Factor	6650765	1	CSVMIFEVVEQAGAIILEDGQELDSWYVILNGTVEISHPD GKVENLFMGNSFGITPTLDKQYMHGIVRTKVDDCQFVCI AQQDYWRILNHVEKNTHKVEEEGEIVMVHEFIVTD	249
HEMBA 1000505	10436367	1	LENVIAKSLLIKSNEGSYGFGLEDKNKVPIIKLVEKGSNAE MAGMEVGKKIFAINGDLVFMRPFNEVDCFLKSCLNSRKP LRVLVSTKP	250
HEMBA 1000505	10436367	2	PRETVKIPDSADGLGFQIRGFGPSVVHAVGRGTVAAAAG LHPGQCIIKVNGINVSKETHASVIAHVTACRKYRRPTKQD SIQNSS	251
HEMBA 1003117	7022001	1	EDFCYVFTVELERGPSGLGMGLIDGMHTHLGAPGLYIQT LLPGSPAAADGRLSLGDRILEVNGSSLLGLGYLRAVDLIR HGGKKMRFLVAKSDVETAKKI	252
HSPC227	7106843	1	NNELTQFLPRTITLKKPPGAQLGFNIRGGKASQLGIFISKVI PDSDAHRAGLQEGDQVLAVNDVDFQDIEHSKAVEILKTA REISMRVRFFPYNYHRQKE	253
HTRA3	AY040094	1	LTEFQDKQIKDWKKRFIGIRMRTITPSLVDELKASNPDFPE VSSGIYVQEVAPNSPSQRGGIQDGDIIVKVNGRPLVDSSEL QEAVLTESPLLLEVRRGNDDLLFSNSS (SEQ ID NO:158)	254
HTRA4	AL576444	1	HKKYLGLQMLSLTVPLSEELKMHYPDFPDVSSGVYVCKV VEGTAAQSSGLRDHDVIVNINGKPITTTTDVVKALDSDSL SMAVLRGKDNLLLTVNSS	255
INADL	2370148	1	IWQIEYIDIERPSTGGLGFSVVALRSQNLGKVDIFVKDVQP GSVADRDQRLKENDQILAINHTPLDQNISHQQAIALLQQT TGSLRLIVAREPVHTKSSTSSSE	256

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
INADL	2370148	2	LPETVCWGHVEEVELINDGSGLGFGIVGGKTSGVVVRTIV PGGLADRDGRLQTGDHILKIGGTNVQGMTSEQVAQVLR NCGNSVRMLVARDPAGDISVTNSS	257
INADL	2370148	3	PGSDSSLFETYNVELVRKDGQSLGIRIVGYVGTSHTGEAS GIYVKSIIPGSAAYHNGHIQVNDKIVAVDGVNIQGFANHD VVEVLRNAGQVVHLTLVRRKTSSSTSRIHRD	258
INADL	2370148	4	NSDDAELQKYSKLLPIHTLRLGVEVDSFDGHHYISSIVSG GPVDTLGLLQPEDELLEVNGMQLYGKSRREAVSFLKEVP PPFTLVCCRRLFDDEAS	259
INADL	2370148	5	LSSPEVKIVELVKDCKGLGFSILDYQDPLDPTRSVIVIRSLV ADGVAERSGGLLPGDRLVSVNEYCLDNTSLAEAVEILKA VPPGLVHLGICKPLVEFIVTD	260
INADL	2370148	6	PNFSHWGPPRIVEIFREPNVSLGISIVVGQTVIKRLKNGEEL KGIFIKQVLEDSPAGKTNALKTGDKILEVSGVDLQNASHS EAVEAIKNAGNPVVFIVQSLSSTPRVIPNVHNKANSS	261
INADL	2370148	7	PGELHIIELEKDKNGLGLSLAGNKDRSRMSIFVVGINPEGP AAADGRMRIGDELLEINNQILYGRSHQNASAIIKTAPSKV KLVFIRNEDAVNQMANSS	262
INADL	2370148	8	PATCPIVPGQEMIIEISKGRSGLGLSIVGGKDTPLNAIVIHE VYEEGAAARDGRLWAGDQILEVNGVDLRNSSHEEAITAL RQTPPQKVRLVVY	263
KIAA0147	1469875	1	ILTLTILRQTGGLGISIAGGKGSTPYKGDDEGIFISRVSEEG PAARAGVRVGDKLLEVNGVALQGAEHHEAVEALRGAGT AVQMRVWRERMVEPENAEFIVTD	264
KIAA0147	1469875	2	PLRQRHVACLARSERGLGFSIAGGKGSTPYRAGDAGIFVS RIAEGGAAHRAGTLQVGDRVLSINGVDVTEARHDHAVSL LTAASPTIALLLEREAGG	265
KIAA0147	1469875	3	ILEGPYPVEEIRLPRAGGPLGLSIVGGSDHSSHPFGVQEPG VFISKVLPRGLAARSGLRVGDRILAVNGQDVRDATHQEA VSALLRPCLELSLLVRRDPAEFIVTD	266
KIAA0147	1469875	4	RELCIQKAPGERLGISIRGGARGHAGNPRDPTDEGIFISKV SPTGAAGRDGRLRVGLRLLEVNQQSLLGLTHGEAVQLLR SVGDTLTVLVCDGFEASTDAALEVS	267
KIAA0303	2224546	1	PHQPIVIHSSGKNYGFTIRAIRVYVGDSDIYTVHHIVWNVE EGSPACQAGLKAGDLITHINGEPVHGLVHTEVIELLLKSG NKVSITTTPF	268
KIAA0313	7657260	1	HLRLLNIACAAKAKRRLMTLTKPSREAPLPFILLGGSEKG FGIFVDSVDSGSKATEAGLKRGDQILEVNGQNFENIQLSK AMEILRNNTHLSITVKTNLFVFKELLTRLSEEKRNGAPNSS	269
KIAA0316	6683123	1	IPPAPRKVEMRRDPVLGFGFVAGSEKPVVVRSVTPGGPSE GKLIPGDQIVMINDEPVSAAPRERVIDLVRSCKESILLTVIQ PYPSPKSEFIVTD	270
KIAA0340	2224620	1	LNKRTTMPKDSGALLGLKVVGGKMTDLGRLGAFITKVK KGSLADVVGHLRAGDEVLEWNGKPLPGATNEEVYNIILE SKSEPQVEIIVSRPIGDIPRIHRD	271
KIAA0380	2224700	1	QRCVIIQKDQHGFGFTVSGDRIVLVQSVRPGGAAMKAGV KEGDRIIKVNGTMVTNSSHLEVVKLIKSGAYVALTLLGSS	272

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
KIAA0382	7662087	1	ILVQRCVIIQKDDNGFGLTVSGDNPVFVQSVKEDGAAMR AGVQTGDRIIKVNGTLVTHSNHLEVVKLIKSGSYVALTV QGRPPGNSS	273
KIAA0440	2662160	1	SVEMTLRRNGLGQLGFHVNYEGIVADVEPYGYAWQAGL RQGSRLVEICKVAVATLSHEQMIDLLRTSVTVKVVIIPPH D	274
KIAA0545	14762850	1	LKVMTSGWETVDMTLRRNGLGQLGFHVKYDGTVAEVE DYGFAWQAGLRQGSRLVEICKVAVVTLTHDQMIDLLRTS VTVKVVIIPPFEDGTPRRGW (SEQ ID NO:179)	275
KIAA0559	3043641	1	HYIFPHARIKITRDSKDHTVSGNGLGIRIVGGKEIPGHSGEI GAYIAKILPGGSAEQTGKLMEGMQVLEWNGIPLTSKTYE EVQSIISQQSGEAEICVRLDLNML	276
KIAA0561	3043645	1	LCGSLRPPIVIHSSGKKYGFSLRAIRVYMGDSDVYTVHHV VWSVEDGSPAQEAGLRAGDLITHINGESVLGLVHMDVVE LLLKSGNKISLRTTALENTSIKVGNSS	277
KIAA0613	3327039	1	SYSVTLTGPGPWGFRLQGGKDFNMPLTISRITPGSKAAQS QLSQGDLVVAIDGVNTDTMTHLEAQNKIKSASYNLSLTL QKSKNSS	278
KIAA0751 RIM2	12734165	1	TLNEEHSHSDKHPVTWQPSKDGDRLIGRILLNKRLKDGS VPRDSGAMLGLKVVGGKMTESGRLCAFITKVKKGSLAD TVGHLRPGDEVLEWNGRLLQGATFEEVYNIILESKPEPQV ELVVSRPIG	279
KIAA0807	3882334	1	ISALGSMRPPIIIHRAGKKYGFTLRAIRVYMGDSDVYTVH HMVWHVEDGGPASEAGLRQGDLITHVNGEPVHGLVHTE VVELILKSGNKVAISTTPLENSS	280
KIAA0858	4240204	1	FSDMRISINQTPGKSLDFGFTIKWDIPGIFVASVEAGSPAEF SQLQVDDEIIAINNTKFSYNDSKEWEEAMAKAQETGHLV MDVRRYGKAGSPE	281
KIAA0902	4240292	1	QSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSP ADRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPS GVILTLKKRPQSMLTSAPA	282
KIAA0967	4589577	1	ILTQTLIPVRHTVKIDKDTLLQDYGFHISESLPLTVVAVTA GGSAHGKLFPGDQILQMNNEPAEDLSWERAVDILREAED SLSITVVRCTSGVPKSSNSS	283
KIAA0973	4589589	1	GLRSPITIQRSGKKYGFTLRAIRVYMGDTDVYSVHHIVWH VEEGGPAQEAGLCAGDLITHVNGEPVHGMVHPEVVELIL KSGNKVAVTTTPFE	284
KIAA1095	5889526	1	QGEETKSLTLVLHRDSGSLGFNIIGGRPSVDNHDGSSSEGI FVSKIVDSGPAAKEGGLQIHDRIIEVNGRDLSRATHDQAV EAFKTAKEPIVVQVLRRTPRTKMFTP	285
KIAA1095	5889526	2	QEMDREELELEEVDLYRMNSQDKLGLTVCYRTDDEDDI GIYISEIDPNSIAAKDGRIREGDRIIQINGIEVQNREEAVALL TSEENKNFSLLIARPELQLD	286
KIAA1202	6330421	1	RSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGG KAALSQKMRTGDELVNINGTPLYGSRQEALILIKGSFRILK LIVRRRNAPVS	287
KIAA1222	6330610	1	ILEKLELFPVELEKDEDGLGISIIGMGVGADAGLEKLGIFV KTVTEGGAAQRDGRIQVNDQIVEVDGISLVGVTQNFAAT	288

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			VLRNTKGNVRFVIGREKPGQVS	
KIAA1284	6331369	1	KDVNVYVNPKKLTVIKAKEQLKLLEVLVGIIHQTKWSWR RTGKQGDGERLVVHGLLPGGSAMKSGQVLIGDVLVAVN DVDVTTENIERVLSCIPGPMQVKLTFENAYDVKRET	289
KIAA1389	7243158	1	TRGCETVEMTLRRNGLGQLGFHVNFEGIVADVEPFGFAW KAGLRQGSRLVEICKVAVATLTHEQMIDLLRTSVTVKVVI IQPHDDGSPRR	290
KIAA1415	7243210	1	VENILAKRLLILPQEEDYGFDIEEKNKAVVVKSVQRGSLA EVAGLQVGRKIYSINEDLVFLRPFSEVESILNQSFCSRRPL RLLVATKAKEIIKIP (SEQ ID NO:195)	291
KIAA1526	5817166	1	PDSAGPGEVRLVSLRRAKAHEGLGFSIRGGSEHGVGIYVS LVEPGSLAEKEGLRVGDQILRVNDKSLARVTHAEAVKAL KGSKKLVLSVYSAGRIPGGYVTNHIEFIVTD	292
KIAA1526	5817166	2	LQGGDEKKVNLVLGDGRSLGLTIRGGAEYGLGIYITGVDP GSEAEGSGLKVGDQILEVNWRSFLNILHDEAVRLLKSSRH LILTVKDVGRLPHARTTVDEEFIVTD	293
KIAA1526	5817166	3	WTSGAHVHSGPCEEKCGHPGHRQPLPRIVTIQRGGSAHN CGQLKVGHVILEVNGLTLRGKEHREAARIIAEAFKTKDR DYIDFLDSL	294
KIAA1620	10047316	1	ELRRAELVEIIVETEAQTGVSGINVAGGGKEGIFVRELRED SPAARSLSLQEGDQLLSARVFFENFKYEDALRLLQCAEPY KVSFCLKRTVPTGDLALRP	295
KIAA1634	10047344	1	PSQLKGVLVRASLKKSTMGFGFTIIGGDRPDEFLQVKNVL KDGPAAQDGKIAPGDVIVDINGNCVLGHTHADVVQMFQ LVPVNQYVNLTLCRGYPLPDDSED	296
KIAA1634	10047344	2	ASSGSSQPELVTIPLIKGPKGFGFAIADSPTGQKVKMILDS QWCQGLQKGDIIKEIYHQNVQNLTHLQVVEVLKQFPVGA DVPLLILRGGPPSPTKTAKM	297
KIAA1634	10047344	3	LYEDKPPLTNTFLISNPRTTADPRILYEDKPPNTKDLDVFL RKQESGFGFRVLGGDGPDQSIYIGAIIPLGAAEKDGRLRA ADELMCIDGIPVKGKSHKQVLDLMTTAARNGHVLLTVR RKIFYGEKQPEDDSGSPGIHRELT	298
KIAA1634	10047344	4	PAPQEPYDVVLQRKENEGFGFVILTSKNKPPPGVIPHKIGR VIEGSPADRCGKLKVGDHISAVNGQSIVELSHDNIVQLIK DAGVTVTLTVIAEEEHHGPPS	299
KIAA1634	10047344	5	QNLGCYPVELERGPRGFGFSLRGGKEYNMGLFILRLAED GPAIKDGRIHVGDQIVEINGEPTQGITHTRAIELIQAGGNK VLLLLRPGTGLIPDHGLA	300
KIAA1719	1267982	0	ITVVELIKKEGSTLGLTISGGTDKDGKPRVSNLRPGGLAA RSDLLNIGDYIRSVNGIHLTRLRHDEIITLLKNVGERVVLE VEY	301
KIAA1719	1267982	1	ILDVSLYKEGNSFGFVLRGGAHEDGHKSRPLVLTYVRPG GPADREGSLKVGDRLLSVDGIPLHGASHATALATLRQCS HEALFQVEYDVATP	302
KIAA1719	1267982	2	IHTVANASGPLMVEIVKTPGSALGISLTTTSLRNKSVITIDR IKPASVVDRSGALHPGDHILSIDGTSMEHCSLLEATKLLAS ISEKVRLEILPVPQSQRPL	303

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
KIAA1719	1267982	3	IQIVHTETTEVVLCGDPLSGFGLQLQGGIFATETLSSPPLV CFIEPDSPAERCGLLQVGDRVLSINGIATEDGTMEEANQL LRDAALAHKVVLEVEFDVAESV	304
KIAA1719	1267982	4	IQFDVAESVIPSSGTFHVKLPKKRSVELGITISSASRKRGEP LIISDIKKGSVAHRTGTLEPGDKLLAIDNIRLDNCPMEDAV QILRQCEDLVKLKIRKDEDN	305
KIAA1719	1267982	5	IQTTGAVSYTVELKRYGGPLGITISGTEEPFDPIVISGLTKR GLAERTGAIHVGDRILAINNVSLKGRPLSEAIHLLQVAGE TVTLKIKKQLDR)	306
KIAA1719	1267982	6	ILEMEELLLPTPLEMHKVTLHKDPMRHDFGFSVSDGLLEK GVYVHTVRPDGPAHRGGLQPFDRVLQVNHVRTRDFDCC LAVPLLAEAGDVLELIISRKPHTAHSS	307
LIM Mystique	12734250	1	MALTVDVAGPAPWGFRITGGRDFHTPIMVTKVAERGKA KDADLRPGDIIVAINGESAEGMLHAEAQSKIRQSPSPLRLQ LDRSQATSPGQT	308
LIM Protein	3108092	1	SNYSVSLVGPAPWGFRLQGGKDFNMPLTISSLKDGGKAA QANVRIGDVVLSIDGINAQGMTHLEAQNKIKGCTGSLNM TLQRAS	309
LIMK1	4587498	1	TLVEHSKLYCGHCYYQTVVTPVIEQILPDSPGSHLPHTVT LVSIPASSHGKRGLSVSIDPPHGPPGCGTEHSHTVRVQGV DPGCMSPDVKNSIHVGDRILEINGTPIRNVPLDEIDLLIQET SRLLQLTLEHD	310
LIMK2	1805593	1	PYSVTLISMPATTEGRRGFSVSVESACSNYATTVQVKEVN RMHISPNNRNAIHPGDRILEINGTPVRTLRVEEVEDAISQT SQTLQLLIEHD	311
LIM-RIL	1085021	1	IHSVTLRGPSPWGFRLVGRDFSAPLTISRVHAGSKASLAA LCPGDLIQAINGESTELMTHLEAQNRIKGCHDHLTLSVSR PE	312
LU-1	U52111	1	VCYRTDDEEDLGIYVGEVNPNSIAAKDGRIREGDRIIQING VDVQNREEAVAILSQEENTNISLLVARPESQLA	313
MAGI1	3370997	1	PSELKGKFIHTKLRKSSRGFGFTVVGGDEPDEFLQIKSLVL DGPAALDGKMETGDVIVSVNDTCVLGHTHAQVVKIFQSI PIGASVDLELCRGYPLPFDPDGIHRD	314
MAGI1	3370997	2	PATQPELITVHIVKGPMGFGFTIADSPGGGGQRVKQIVDSP RCRGLKEGDLIVEVNKKNVQALTHNQVVDMLVECPKGS EVTLLVQRGGNSSZ	315
MAGI1	3370997	3	QATQEQDFYTVELERGAKGFGFSLRGGREYNMDLYVLR LAEDGPAERCGKMRIGDEILEINGETTKNMKHSRAIELIK NGGRRVRLFLKRG	316
MAGI1	3370997	4	PGVVSTVVQPYDVEIRRGENEGFGFVIVSSVSRPEAGTTF AGNACVAMPHKIGRIIEGSPADRCGKLKVGDRILAVNGC SITNKSHSDIVNLIKEAGNTVTLRIIPGDESSNAEFIVTD	317
MAGI1	3370997	5	PDYQEQDIFLWRKETGFGFRILGGNEPGEPIYIGHIVPLGA ADTDGRLRSGDELICVDGTPVIGKSHQLVVQLMQQAAKQ GHVNLTVRRKVVFAVPKTENSS	318
MGC5395	BC012477	1	PAKMEKEETTRELLLPNWQGSGSHGLTIAQRDDGVFVQE VTQNSPAARTGVVKEGDQIVGATIYFDNLQSGEVTQLLN TMGHHTVGLKLHRKGDRSPNSS	319

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
MINT1	2625024	1	SENCKdVFIEKQKGEILGVVIVESGWGSILPTVIIANMMHG GPAEKSGKLNIGDQIMSINGTSLVGLPLSTCQSIIKGLKNQ SRVKLNIVRCPPVNSS	320
MINT1	2625024	2	LRCPPVTTVLIRRPDLRYQLGFSVQNGIICSLMRGGIAERG GVRVGHRIIEINGQSVVATPHEKIVHILSNAVGEIHMKTM PAAMYRLLNSS	321
MINT3	3169808	1	HNGDLDHFSNSDNCREVHLEKRRGEGLGVALVESGWGS LLPTAVIANLLHGGPAERSGALSIGDRLTAINGTSLVGLPL AACQAAVRETKSQTSVTLSIVHCPPVT	322
MINT3	3169808	2	PVTTAIIHRPHAREQLGFCVEDGIICSLLRGGIAERGGIRVG HRIIEINGQSVVATPHARIIELLTEAYGEVHIKTMPAATYR LLTG NSS	323
MPP1	189785	1	RKVRLIQFEKVTEEPMGITLKLNEKQSCTVARILHGGMIH RQGSLHVGDEILEINGTNVTNHSVDQLQKAMKETKGMIS LKVIPNQ	324
MPP2	939884	1	PVPPDAVRMVGIRKTAGEHLGVTFRVEGGELVIARILHGG MVAQQGLLHVGDIIKEVNGQPVGSDPRALQELLRNASGS VILKILPNYQ	325
MPP3	1022812	1	NIDEDFDEESVKIVRLVKNKEPLGATIRRDEHSGAVVVAR IMRGGAADRSGLVHVGDELREVNGIAVLHKRPDEISQILA QSQGSITLKIIPATQEEDR	326
MUPP1	2104784	1	QGRHVEVFELLKPPSGGLGFSVVGLRSENRGELGIFVQEI QEGSVAHRDGRLKETDQILAINGQALDQTITHQQAISILQ KAKDTVQLVIARGSLPQLV	327
MUPP1	2104784	2	PVHWQHMETIELVNDGSGLGFGIIGGKATGVIVKTILPGG VADQHGRLCSGDHILKIGDTDLAGMSSEQVAQVLRQCG NRVKLMIARGAIEERTAPT	328
MUPP1	2104784	3	QESETFDVELTKNVQGLGITIAGYIGDKKLEPSGIFVKSIT KSSAVEHDGRIQIGDQIIAVDGTNLQGFTNQQAVEVLRHT GQTVLLTLMRRGMKQEA	329
MUPP1	2104784	4	LNYEIVVAHVSKFSENSGLGISLEATVGHHFIRSVLPEGPV GHSGKLFSGDELLEVNGITLLGENHQDVVNILKELPIEVT MVCCRRTVPPT	330
MUPP1	2104784	5	WEAGIQHIELEKGSKGLGFSILDYQDPIDPASTVIIRSLVP GGIAEKDGRLLPGDRLMFVNDVNLENSSLEEAVEALKGA PSGTVRIGVAKPLPLSPEENSS	331
MUPP1	2104784	6	RNVSKESFERTINIAKGNSSLGMTVSANKDGLGMIVRSIIH GGAISRDGRIAIGDCILSINEESTISVTNAQARAMLRRHSLI GPDIKITYVPAEHLEE	332
MUPP1	2104784	7	LNWNQPRRVELWREPSKSLGISIVGGRGMGSRLSNGEVM RGIFIKHVLEDSPAGKNGTLKPGDRIVEVDGMDLRDASHE QAVEAIRKAGNPVVFMVQSIINRPRKSPLPSLL	333
MUPP1	2104784	8	LTGELHMIELEKGHSGLGLSLAGNKDRSRMSVFIVGIDPN GAAGKDGRLQIADELLEINGQILYGRSHQNASSIIKCAPSK VKIIFIRNKDAVNQ	334
MUPP1	2104784	9	LSSFKNVQHLELPKDQGGLGIAISEEDTLSGVIIKSLTEHG VAATDGRLKVGDQILAVDDEIVVGYPIEKFISLLKTAKMT VKLTIHAENPDSQ	335

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
MUPP1	2104784	10	LPGCETTIEISKGRTGLGLSIVGGSDTLLGAIIIHEVYEEGA ACKDGRLWAGDQILEVNGIDLRKATHDEAINVLRQTPQR VRLTLYRDEAPYKE	336
MUPP1	2104784	11	KEEEVCDTLTIELQKKPGKGLGLSIVGKRNDTGVFVSDIV KGGIADADGRLMQGDQILMVNGEDVRNATQEAVAALLK CSLGTVTLEVGRIKAGPFHS	337
MUPP1	2104784	12	LQGLRTVEMKKGPTDSLGISIAGGVGSPLGDVPIFIAMMH PTGVAAQTQKLRVGDRIVTICGTSTEGMTHTQAVNLLKN ASGSIEMQVVAGGDVSV	338
MUPP1	2104784	13	LGPPQCKSITLERGPDGLGFSIVGGYGSPHGDLPIYVKTVF AKGAASEDGRLKRGDQIIAVNGQSLEGVTHEEAVAILKR TKGTVTLMVLS	339
NeDLG	10863920	1	IQYEEIVLERGNSGLGFSIAGGIDNPHVPDDPGIFITKIIPGG AAAMDGRLGVNDCVLRVNEVEVSEVVHSRAVEALKEA GPVVRLVVRRRQN	340
NeDLG	10863920	2	ITLLKGPKGLGFSIAGGIGNQHIPGDNSIYITKIIEGGAAQK DGRLQIGDRLLAVNNTNLQDVRHEEAVASLKNTSDMVY LKVAKPGSLE	341
NeDLG	10863920	3	ILLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELR RGDRILSVNGVNLRNATHEQAAAALKRAGQSVTIVAQYR PEEYSRFESKIHDLREQMMNSSMSSGSGSLRTSEKRSLE	342
Neurabin II	AJ401189	1	CVERLELFPVELEKDSEGLGISIIGMGAGADMGLEKLGIFV KTVTEGGAAHRDGRIQVNDLLVEVDGTSLVGVTQSFAAS VLRNTKGRVRFMIGRERPGEQSEVAQRIHRD (SEQ ID NO:247)	343
NOS1	642525	1	IQPNVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGA AEQSGLIQAGDIILAVNGRPLVDLSYDSALEVLRGIASETH VVLILRGP	344
novel PDZ gene	7228177	1	QANSDESDIIHSVRVEKSPAGRLGFSVRGGSEHGLGIFVSK VEEGSSAERAGLCVGDKITEVNGLSLESTTMGSAVKVLTS SSRLHMMVRRMGRVPGIKFSKEKNSS	345
novel PDZ gene	7228177	2	PSDTSSEDGVRRIVHLYTTSDDFCLGFNIRGGKEFGLGIYV SKVDHGGLAEENGIKVGDQVLAANGVRFDDISHSQAVEV LKGQTHIMLTIKETGRYPAYKEMNSS	346
Novel Serine Protease	1621243	1	KIKKFLTESHDRQAKGKAITKKKYIGIRMMSLTSSKAKEL KDRHRDFPDVISGAYIIEVIPDTPAEAGGLKENDVIISINGQ SVVSANDVSDVIKRESTLNMVVRRGNEDIMITV	347
Numb Binding Protein	AK056823	1	PDGEITSIKINRVDPSESLSIRLVGGSETPLVHIIIQHIYRDG VIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQV LWLTVMREQKFRSRNSS	348
Numb Binding Protein	AK056823	2	HRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLD GGVAYRHGQLEENDRVLAINGHDLRYGSPESAAHLIQAS ERRVHLVVSRQVRQRSPENSS	349
Numb Binding Protein	AK056823	3	PTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVI SVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALL KRTSSSIVLKALEVKEYEPQEFIV	350
Outer Membrane	7023825	1	LLTEEEINLTRGPSGLGFNIVGGTDQQYVSNDSGIYVSRIK ENGAAALDGRLQEGDKILSVNGQDLKNLLHQDAVDLFR	351

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			NAGYAVSLRVQHRLQVQNGIHS	
p55T	12733367	1	PVDAIRILGIHKRAGEPLGVTFRVENNDLVIARILHGGMID RQGLLHVGDIIKEVNGHEVGNNPKELQELLKNISGSVTLK ILPSYRDTITPQQ	352
PAR3	8037914	1	PNFSLDDMVKLVEVPNDGGPLGIHVVPFSARGGRTLGLL VKRLEKGGKAEHENLFRENDCIVRINDGDLRNRRFEQAQ HMFRQAMRTPIIWFHVVPAANKEQYEQ	353
PAR3	8037914	2	GKRLNIQLKKGTEGLGFSITSRDVTIGGSAPIYVKNILPRG AAIQDGRLKAGDRLIEVNGVDLVGKSQEEVVSLLRSTKM EGTVSLLVFRQEDA	354
PAR3	8037914	3	PREFLTFEVPLNDSGSAGLGVSVKGNRSKENHADLGIFVK SIINGGAASKDGRLRVNDQLIAVNGESLLGKTNQDAMET LRRSMSTEGNKRGMIQLIVASRISKCNELKSNSS	355
PAR3-like	AF428250	1	PRTKDTLSDMTRTVEISGEGGPLGIHVVPFFSSLSGRILGLF IRGIEDNSRSKREGLFHENECIVKINNVDLVDKTFAQAQD VFRQAMKSPSVLLHVLPPQNR	356
PAR3-like	AF428250	2	SNKNAKKIKIDLKKGPEGLGFTVVTRDSSIHGPGPIFVKNI LPKGAAIKDGRLQSGDRILEVNGRDVTGRTQEELVAMLR STKQGETASLVIARQEGH	357
PAR3-like	AF428250	3	ITSEQLTFEIPLNDSGSAGLGVSLKGNKSRETGTDLGIFIKS IIHGGAAFKDGRLRMNDQLIAVNGESLLGKSNHEAMETL RRSMSMEGNIRGMIQLVILRRPERP	358
PAR6	2613011	1	PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQGLERVP GIFISRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLDQV TDMMVANSHNLIVTVKPANQRNNVNSS	359
PAR6 BETA	13537116	1	PVSSIIDVDILPETHRRVRLYKYGTEKPLGFYIRDGSSVRV TPHGLEKVPGIFISRLVPGGLAQSTGLLAVNDEVLEVNGIE VSGKSLDQVTDMMIANSRNLIITVRPANQRNNRIHRD	360
PAR6 GAMMA	13537118	1	IDVDLVPETHRRVRLHRHGCEKPLGFYIRDGASVRVTPHG LEKVPGIFISRMVPGGLAESTGLLAVNDEVLEVNGIEVAG KTLDQVTDMMIANSHNLIVTVKPANQRNNVV	361
PDZ-73	5031978	1	RSRKLKEVRLDRLHPEGLGLSVRGGLEFGCGLFISHLIKG GQADSVGLQVGDEIVRINGYSISSCTHEEVINLIRTKKTVSI KVRHIGLIPVKSSPDEFH	362
PDZ-73	5031978	2	IPGNRENKEKKVFISLVGSRGLGCSISSGPIQKPGIFISHVKP GSLSAEVGLEIGDQIVEVNGVDFSNLDHKEAVNVLKSSRS LTISIVAAAGRELFMTDEF	363
PDZ-73	5031978	3	PEQIMGKDVRLLRIKKEGSLDLALEGGVDSPIGKVVVSAV YERGAAERHGGIVKGDEIMAINGKIVTDYTLAEADAALQ KAWNQGGDWIDLVVAVCPPKEYDD	364
PDZK1	2944188	1	LTSTFNPRECKLSKQEGQNYGFFLRIEKDTEGHLVRVVEK CSPAEKAGLQDGDRVLRINGVFVDKEEHMQVVDLVRKS GNSVTLLVLDGDSYEKAGSPGIHRD	365
PDZK1	2944188	2	RLCYLVKEGGSYGFSLKTVQGKKGVYMTDITPQGVAMR AGVLADDHLIEVNGENVEDASHEEVVEKVKKSGSRVMF LLVDKETDKREFIVTD	366
PDZK1	2944188	3	QFKRETASLKLLPHQPRIVEMKKGSNGYGFYLRAGSEQK	367

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			GQIIKDIDSGSPAEEAGLKNNDLVVAVNGESVETLDHDSV VEMIRKGGDQTSLLVVDKETDNMYRLAEFIVTD	
PDZK1	2944188	4	PDTTEEVDHKPKLCRLAKGENGYGFHLNAIRGLPGSFIKE VQKGGPADLAGLEDEDVIIEVNGVNVLDEPYEKVVDRIQ SSGKNVTLLVZGKNSS	368
PICK1	4678411	1	PTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNT PAALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKG EVTIHYNKLQ	369
PIST	98374330	1	SQGVGPIRKVLLLKEDHEGLGISITGGKEHGVPILISEIHPG QPADRCGGLHVGDAILAVNGVNLRDTKHKEAVTILSQQR GEIEFEVVYVAPEVDSD	370
prIL16	1478492	1	IHVTILHKEEGAGLGFSLAGGADLENKVITVHRVFPNGLA SQEGTIQKGNEVLSINGKSLKGTTHHDALAILRQAREPRQ AVIVTRKLTPEEFIVTD	371
prIL16	1478492	2	TAEATVCTVTLEKMSAGLGFSLEGGKGSLHGDKPLTINRI FKGAASEQSETVQPGDEILQLGGTAMQGLTRFEAWNIIKA LPDGPVTIVIRRKSLQSK	372
PSAP	6409315		IREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGDVVFLW GCNLLAHFINAYLVDDSVSDTPGGLGNDQNPGSQFSQAL AIRSYTKFVMGIAVSMLTYPFLLVGDLMAVNNCGLQAGL PPYSPVFKSWIHCWKYLSVQGQLFRGSSLLFRRVSSGSCF ALE	373
PSD95	3318652	1	LEYEeITLERGNSGLGFSIAGGTDNPHIGDDPSIFITKIIPGG AAAQDGRLRVNDSILFVNEVDVREVTHSAAVEALKEAGS IVRLYVMRRKPPAENSS	374
PSD95	3318652	2	HVMRRKPPAEKVMEIKLIKGPKGLGFSIAGGVGNQHIPGD NSIYVTKIIEGGAAHKDGRLQIGDKILAVNSVGLEDVMHE DAVAALKNTYDVVYLKVAKPSNAYLLEFIVTD	375
PSD95	3318652	3	RERHTPRTEANCDHRGSTGLGFNIVGGEDGEGILSPLSWP GALQTSVGSCGRGTRSCRSTVWTSEMPAMSRLPLP	376
PTN-3	179912	1	QNDNGDSYLVLIRITPDEDGKFGFNLKGGVDQKMPLVVS RINPESPADTCIPKLNEGDQIVLINGRDISEHTHDQVVMFI KASRESHSRELALVIRRRAVRS	377
PTN-4	190747	1	IRMKPDENGRFGFNVKGGYDQKMPVIVSRVAPGTPADLC VPRLNEGDQVVLINGRDIAEHTHDQVVLFIKASCERHSGE LMLLVRPNA	378
PTPL1	515030	1	PEREITLVNLKKDAKYGLGFQIIGGEKMGRLDLGIFISSVA PGGPADFHGCLKPGDRLISVNSVSLEGVSHHAAIEILQNA PEDVTLVISQPKEKISKVPSTPVHL	379
PTPL1	515030	2	GDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQ GAAESDGRIHKGDRVLAVNGVSLEGATHKQAVETLRNT GQVVHLLLEKGQSPTSK	380
PTPL1	515030	3	TEENTFEVKLFKNSSGLGFSFSREDNLIPEQINASIVRVKK LFAGQPAAESGKIDVGDVILKVNGASLKGLSQQEVISALR GTAPEVFLLLCRPPPGVLPEIDT	381
PTPL1	515030	4	ELEVELLITLIKSEKASLGFTVTKGNQRIGCYVHDVIQDPA KSDGRLKPGDRLIKVNDTDVTNMTHTDAVNLLRAASKT VRLVIGRVLELPRIPMLPH	382

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
PTPL1	515030	5	MLPHLLPDITLTCNKEELGFSLCGGHDSLYQVVYISDINPR SVAAIEGNLQLLDVIHYVNGVSTQGMTLEEVNRALDMSL PSLVLKATRNDLPV	383
RGS12	3290015	1	RPSPPRVRSVEVARGRAGYGFTLSGQAPCVLSCVMRGSP ADFVGLRAGDQILAVNEINVKKASHEDVVKLIGKCSGVL HMVIAEGVGRFESCSNSS	384
RGS3	18644735	1	LCSERRYRQITIPRGKDGFGFTICCDSPVRVQAVDSGGPAE RAGLQQLDTVLQLNERPVEHWKCVELAHEIRSCPSEIILL VWRMVPQVKPGIHRD	385
Rho-GAP 10	NM020824	1	SEDETFSWPGPKTVTLKRTSQGFGFTLRHFIVYPPESAIQF SYKDEENGNRGGKQRNRLEPMDTIFVKQVKEGGPAFEA GLCTGDRIIKVNGESVIGKTYSQVIALIQNSDTTLELSVMP KDED	386
Rhophilin-like	14279408	1	SAKNRWRLVGPVHLTRGEGGFGLTLRGDSPVLIAAVIPGS QAAAAGLKEGDYIVSVNGQPCRWWRHAEVVTELKAAG EAGASLQVVSLLPSSRLPSI	387
Serine Protease	2738914	1	RGEKKNSSSGISGSQRRYIGVMMLTLSPSILAELQLREPSF PDVQHGVLIHKVILGSPAHRAGLRPGDVILAIGEQMVQN AEDVYEAVRTQSQLAVQIRRGRETLTLYVNSS	388
Shank 2	6049185	1	LEEKTVVLQKKDNEGFGFVLRGAKADTPIEEFTPTPAFPA LQYLESVDEGGVAWQAGLRTGDFLIEVNNENVVKVGHR QVVNMIRQGGNHLVLKVVTVTRNLDPDDNSS	389
Shank 3	*	1	SDYVIDDKVAVLQKRDHEGFGFVLRGAKAETPIEEFTPTP AFPALQYLESVDVEGVAWRAGLRTGDFLIEVNGVNVVK VGHKQVVALIRQGGNRLVMKVVSVTRKPEEDG	390
Shroom	18652858	1	ISNTATKGRYIYLEAFLEGGAPWGFTLKGGLEHGEPLIISK VEEGGKADTLSSKLQAGDEVVHINEVTLSSSRKEAVSLV KGSYKTLRLVVRRDVCTDPGHAD	391
Similar to GRASP65	14286261	1	MGLGVSAEQPAGGAEGFHLHGVQENSPAQQAGLEPYFD FIITIGHSRLNKENDTLKALLKANVEKPVKLEVFNMKTMR VREVEVVPSNMWGGQGLLGASVRFCSFRRASE	392
Similar to GRASP65	14286261	2	RASEQVWHVLDVEPSSPAALAGLRPYTDYVVGSDQILQE SEDFFTLIESHEGKPLKLMVYNSKSDSCRESGMWHWLW VSTPDPNSAPQLPQEATWHPTTFCSTTWCPTT	393
Similar to Ligand of Numb px2	BC036755	1	IQPLSLPEGEITTIEIHRSNPYIQLGISIVGGNETPLINIVIQEV YRDGVIARDGRLLAGDQILQVNNYNISNVSHNYARAVLS QPCNTLHLTVLRERRFGNRAH	394
Similar to Ligand of Numb px2	BC036755	2	SNSPREEIFQVALHKRDSGEQLGIKLVRRTDEPGVFILDLL EGGLAAQDGRLSSNDRVLAINGHDLKYGTPELAAQIIQAS GERVNLTIARPGKPQPG	395
Similar to Ligand of Numb px2	BC036755	3	QCVTCQEKHITVKKEPHESLGMTVAGGRGSKSGELPIFVT SVPPHGCLARDGRIKRGDVLLNINGIDLTNLSHSEAVAML KASAASPAVALKALEVQIVEEAT	396
Similar to Ligand of Numb px2	BC036755	4	PSTLHSCHDIVLRRSYLGSWGFSIVGGYEENHTNQPFFIKT IVLGTPAYYDGRLKCGDMIVAVNGLSTVGMSHSALVPM LKEQRNKVTLTVICWPGS	397
Similar to PTP	21595065	1	SVTDGPKFEVKLKKNANGLGFSFVQMEKESCSHLKSDLV RIKRLFPGQPAEENGAIAAGDIILAVNGRSTEGLIFQEVLH	398

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
Homolog			LLRGAPQEVTLLLCRPPPGA	
SIP1	2047327	1	QPEPLRPRLCRLVRGEQGYGFHLHGEKGRRGQFIRRVEPG SPAEAAALRAGDRLVEVNGVNVEGETHHQVVQRIKAVE GQTRLLVVDQETDEELRRRNSS	399
SIP1	2047327	2	PLRELRPRLCHLRKGPQGYGFNLHSDKSRPGQYIRSVDPG SPAARSGLRAQDRLIEVNGQNVEGLRHAEVVASIKARED EARLLVVDPETDEHFKRNSS	400
SITAC-18	8886071	1	PGVREIHLCKDERGKTGLRLRKVDQGLFVQLVQANTPAS LVGLRFGDQLLQIDGRDCAGWSSHKAHQVVKKASGDKI VVVVRDRPFQRTVTM	401
SITAC-18	8886071	2	PFQRTVTMHKDSMGHVGFVIKKGKIVSLVKGSSAARNGL LTNHYVCEVDGQNVIGLKDKKIMEILATAGNVVTLTIIPS VIYEHIVEFIV	402
SNPCIIA	20809633	1	SLERPRFCLLSKEEGKSFGFHLQQELGRAGHVVCRVDPGT SAQRQGLQEGDRILAVNNDVVEHEDYAVVVRRIRASSPR VLLTVLARHAHDVARAQ	403
SNPCIIA	20809633	3	ISLPTKPRCLHLEKGPQGFGFLLREEKGLDGRPGQFLWEV DPGLPAKKAGMQAGDRLVAVAGESVEGLGHEETVSRIQ GQGSCVSLTVVDPEADR	404
SNPCIIA	20809633	4	IPSVPLGSRQCFLYPGPGGSYGFRLSCVASGPRLFISQVTP GGSAARAGLQVGDVILEVNGYPVGGQNDLERLQQLPEA EPPLCLKLAARSLRGLE	405
Shank1	7025450	1	LKEKTVLLQKKDSEGFGFVLRGAKAQTPIEEFTPTPAFPA LQYLESVDEGGVAWRAGLRMGDFLIEVNGQNVVKVGH RQVVNMIRQGGNTLMVKVVMVTRHPDMDEAVQNSS	406
SYNTENIN	2795862	1	LEIKQGIREVILCKDQDGKIGLRLKSIDNGIFVQLVQANSP ASLVGLRFGDQVLQINGENCAGWSSDKAHKVLKQAFGE KITMRIHRD	407
SYNTENIN	2795862	2	LRDRPFERTITMHKDSTGHVGFIFKNGKITSIVKDSSAARN GLLTEHNICEINGQNVIGLKDSQIADILSTSGTVVTITMPAF IFEHMNSS	408
Syntrophin 1 alpha	1145727	1	QRRRVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAA DQTEALFVGDAILSVNGEDLSSATHDEAVQVLKKTGKEV VLEVKYMKDVSPYFK	409
Syntrophin beta 2	476700	1	PVRRVVKQEAGGLGISIKGGRENRMPILISKIFPGLAADQS RALRLGDAILSVNGTDLRQATHDQAVQALKRAGKEVLL EVKFIRE	410
Syntrophin gamma 1	9507162	1	EPFYSGERTVTIRRQTVGGFGLSIKGGAEHNIPVVVSKISK EQRAELSGLLFIGDAILQINGINVRKCRHEEVVQVLRNAG EEVTLTVSFLKRAPAFLKLP	411
Syntrophin gamma 2	9507164	1	SHQGRNRRTVTLRRQPVGGLGLSIKGGSEHNVPVVISKIF EDQAADQTGMLFVGDAVLQVNGIHVENATHEEVVHLLR NAGDEVTITVEYLREAPAFLK	412
TAX2-like protein	3253116	1	RGETKEVEVTKTEDALGLTITDNGAGYAFIKRIKEGSIINRI EAVCVGDSIEAINDHSIVGCRHYEVAKMLRELPKSQPFTL RLVQPKRAF	413
TIAM 1	4507500	1	HSIHIEKSDTAADTYGFSLSSVEEDGIRRLYVNSVKETGLA	414

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			SKKGLKAGDEILEINNRAADALNSSMLKDFLSQPSLGLLV RTYPELE	
TIAM 2	6912703	1	PLNVYDVQLTKTGSVCDFGFAVTAQVDERQHLSRIFISDV LPDGLAYGEGLRKGNEIMTLNGEAVSDLDLKQMEALFSE KSVGLTLIARPPDTKATL	415
TIP1	2613001	1	QRVEIHKLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKG IYVTRVSEGGPAEIAGLQIGDKIMQVNGWDMTMVTHDQ ARKRLTKRSEEVVRLLVTRQSLQK	416
TIP2	2613003	1	RKEVEVFKSEDALGLTITDNGAGYAFIKRIKEGSVIDHIHL ISVGDMIEAINGQSLLGCRHYEVARLLKELPRGRTFTLKL TEPRK	417
TIP33	2613007	1	HSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVA ERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDS VKLVVRYTPKVL	418
TIP43	2613011	1	LSNQKRGVKVLKQELGGLGISIKGGKENKMPILISKIFKGL AADQTQALYVGDAILSVNGADLRDATHDEAVQALKRAG KEVLLEVKYMREATPYVKNSS	419
Unknown PDZ gene		1	QRSSIKTVELIKGNLQSVGLTLRLVQSTDGYAGHVIIETVA PNSPAAIADLQRGDRLIAIGGVKITSTLQVLKLIKQAGDRV LVYYERPVGQSNQGA	420
X-11 beta	3005559	1	IHFSNSENCKELQLEKHKGEILGVVVESGWGSILPTVILA NMMNGGPAARSGKLSIGDQIMSINGTSLVGLPLATCQGII KGLKNQTQVKLNIVSCPPVTTVLIKRNSS	421
X-11 beta	3005559	2	IPPVTTVLIKRPDLKYQLGFSVQNGIICSLMRGGIAERGGV RVGHRIIEINGQSVVATAHEKIVQALSNSVGEIHMKTMPA AMFRLLTGQENSS	422
ZO-1	292937	1	IWEQHTVTLHRAPGFGFGIAISGGRDNPHFQSGETSIVISD VLKGGPAEGQLQENDRVAMVNGVSMDNVEHAFAVQQL RKSGKNAKITIRRKKKVQIPNSS	423
ZO-1	292937	2	ISSQPAKPTKVTLVKSRKNEEYGLRLASHIFVKEISQDSLA ARDGNIQEGDVVLKINGTVTENMSLTDAKTLIERSKGKL KMVVQRDRATLLNSS	424
ZO-1	292937	3	IRMKLVKFRKGDSVGLRLAGGNDVGIFVAGVLEDSPAAK EGLEEGDQILRVNNVDFTNIIREEAVLFLLDLPKGEEVTIL AQKKKDVFSN	425
ZO-2	12734763	1	LIWEQYTVTLQKDSKRGFGIAVSGGRDNPHFENGETSIVIS DVLPGGPADGLLQENDRVVMVNGTPMEDVLHSFAVQQL RKSGKVAAIVVKRPRKV	426
ZO-2	12734763	2	RVLLMKSRANEEYGLRLGSQIFVKEMTRTGLATKDGNLH EGDIILKINGTVTENMSLTDARKLIEKSRGKLQLVVLRDS	427
ZO-2	12734763	3	HAPNTKMVRFKKGDSVGLRLAGGNDVGIFVAGIQEGTSA EQEGLQEGDQILKVNTQDFRGLVREDAVLYLLEIPKGEM VTILAQSRADVY	428
ZO-3	10092690	1	IPGNSTIWEQHTATLSKDPRRGFGIAISGGRDRPGGSMVV SDVVPGGPAEGRLQTGDHIVMVNGVSMENATSAFAIQIL KTCTKMANITVKRPRRIHLPAEFIVTD	429
ZO-3	10092690	2	QDVQMKPVKSVLVKRRDSEEFGVKLGSQIFIKHITDSGLA ARHRGLQEGDLILQINGVSSQNLSLNDTRRLIEKSEGKLSL	430

Gene Name	GI or Acc#	PDZ#	Sequence fused to GST Construct	SEQ ID NO:
			LVLRDRGQFLVNIPNSS	
ZO-3	10092690	3	RGYSPDTRVVRFLKGKSIGLRLAGGNDVGIFVSGVQAGSP ADGQGIQEGDQILQVNDVPFQNLTREEAVQFLLGLPPGEE MELVTQRKQDIFWKMVQSEFIVTD	431

*: No GI number for this PDZ domain containing protein - it was computer cloned by J.S. using rat Shank3 seq against human genomic clone AC000036. In silico spliced together nt6400-6496, 6985-7109, 7211-7400 to create hypothetical human Shank3.

At page 49 through page 50, please replace Table 4 with the following Table 4:

TABLE 4

Primers used in cloning of RIM2 PDZ domain 1.

ID# (Primer Name)	Primer Sequence	Description	Seq ID
1968 (688KIFlo)	AAAGATCTCCCTTA ACGAGGAGCATAG	Forward (5' to 3') primer corresponding to RIM2, domain 1. Generates a BglII site upstream (5') of the PDZ boundary. Used for cloning into pGEX-3X.	~~273~~ 432
1093 (319 KIR)	GAACAATTGCAATA GGCCTTGAAACTAC	Reverse (3' to 5') primer corresponding to RIM2, domain 1. Generates a MfeI site downstream (3') of the PDZ boundary. Used for cloning into pGEX-3X.	~~274~~ 434

At page 50, lines 2 through lines 9, please replace the paragraph with the following paragraph:

RIM2, PDZ domain 1: GI#: 12734165; Construct: RIM2, PDZ domain 1-pGEX-3X; primers: 1968 & 1093; Vector Cloning Sites (5'/3'): Bam H1/EcoR1; Insert Cloning Sites(5'/3'): BglII/MfeI

aa 1- aa 126

TLNEEHSHSDKHPVTWQPSKDGDRLIGRILLNKRLKDGSVPRDSGAMLGLKVVGGKMT

ESGRLCAFITKVKKGSLADTVGHLRPGDEVLEWNGRLLQGATFEEVYNIILESKPEPQVE

LVVSRPIG (SEQ ID NO:437)

At page 54 through page 59, please replace Table 5 with the following Table 5

Table 5
Oligonucleotide primers used for RT-PCR

AVC No	Oligo Name	Sequence	SEQ ID NO'	Description
3303	Zo-3 dom3 FA	Gcatccaggagggagatcag	437	forward amplicon primer
3302	Zo-3 dom3 RA	aggttctggaatggcacgtc	438	reverse amplicon primer
3301	Zo-3 dom3 FB	gggcatccaggagggagat	439	forward amplicon primer
3300	Zo-3 dom3 RB	caggttctggaatggcacg	440	reverse amplicon primer
3299	Zo-3 dom1 FA	caggcgaccacatcgtcat	441	forward amplicon primer
3298	Zo-3 dom1 RA	gaggtggcattctccatgga	442	reverse amplicon primer
3297	Zo-3 dom1 FB	tccatggagaatgccacctc	443	forward amplicon primer
3296	Zo-3 dom1 RB	ccatcttggtgcaggtcttga	444	reverse amplicon primer
3295	Zo-2 dom1 FA	agtggtcatggtcaatggca	445	forward amplicon primer
3294	Zo-2 dom1 RA	gcaaacgaatgaagcacatcc	446	reverse amplicon primer
3293	Zo-2 dom1 FB	ctgatgggctgctccaaga	447	forward amplicon primer
3292	Zo-2 dom1 RB	gggtgccattgaccatgac	448	reverse amplicon primer
3291	Zo-2 dom2 FA	agtatggtctccggcttggg	449	forward amplicon primer
3290	Zo-2 dom2 RA	ttcgggtcatttcctttacga	450	reverse amplicon primer
3289	Zo-2 dom2 FB	gatgaaaagcagagcgaacga	451	forward amplicon primer
3288	Zo-2 dom 2 RB	cgaagatctgactcccaagcc	452	reverse amplicon primer
3252	KIA0340 DOM 1 2ND R	caccaagtcgtcctaagtcagtcat	453	reverse amplicon primer
3251	KIA0340 DOM 1 2ND F	tgggtctgaaagttgttggagg	454	forward amplicon primer
3250	GRIP2 DOM 5 2ND R	cagttgtccaggcggatattg	455	reverse amplicon primer
3249	GRIP2 DOM 5 2ND F	ggagccaggcgacaagc	456	forward amplicon primer
3248	LIM MYST DOM 1 2ND R	cgttgatggccacgattatgt	457	reverse amplicon primer
3247	LIM MYST DOM 1 2ND F	aaagccaaggacgctgacct	458	forward amplicon primer
3246	KIA0316 DOM 1 2ND R	aggagtatcgattctttgcagctt	459	reverse amplicon primer
3245	KIA0316 DOM 1 2ND F	cagagagcgggtcatcgatc	460	forward amplicon primer
3244	MAGI2 DOM5 2ND R	tcctaccctcatcctcccatt	461	reverse amplicon primer
3243	MAGI2 DOM5 2ND F	agactggcagaagatggacca	462	forward amplicon primer
3242	MAST1 DOM 1 2ND R	tccgtgtcacccatgtagacac	463	reverse amplicon primer
3241	MAST1 DOM 1 2ND F	gaagtatggcttcacactgcgt	464	forward amplicon primer
3240	MINT3 COMPL 2ND R	catgcctggactccaggct	465	reverse amplicon primer
3239	MINT3 COMPL 2ND F	cgatttgggaactgcctgaa	466	forward amplicon primer
3238	MUPP1 DOM 3 2ND R	caatgtagccagcaatggtaattc	467	reverse amplicon primer
3237	MUPP1 DOM 3 2ND F	gaactcactaaaaatgtccaaggattag	468	forward amplicon primer
3236	NOVEL PDZ DOM 1	ccatggtggtgctctccag	469	reverse amplicon primer

AVC No	Oligo Name	Sequence	SEQ ID NO'	Description
	2ND R			
	NOVEL PDZ DOM 1		470	
3235	2ND F	gggacaagatcacggaggtg		forward amplicon primer
3234	NSP DOM 1 2ND R	cgctcctgagatcacgtctg	471	reverse amplicon primer
3233	NSP DOM 1 2ND F	aaagagctgaaggaccggc	472	forward amplicon primer
3232	HER1 2ND R	tggccatcacgtaggcttc	473	reverse amplicon primer
3231	HER1 2ND F	agcaacatctccgaaagcca	474	forward amplicon primer
	SYNTROPHINY DOM		475	
3230	1 R	tcagctgcttggtcttcgaat		reverse amplicon primer
	SYNTROPHINY DOM		476	
3229	1 F	gcacaacgtccctgtcgtc		forward amplicon pimer
3228	PRIL16 DOM 1 R	cgtggtccccttgagagactt	477	reverse amplicon primer
3227	PRIL16 DOM 1 F	aagggcaatgaggttctttcc	478	forward amplicon primer
3226	KIA 1719 DOM 5 R	gcagttgtccaggcggata	479	reverse amplicon primer
3225	KIA 1719 DOM 5 F	gagccaggcgacaagctact	480	forward amplicon primer
3224	KIA1526 DOM 1 R	cccgcagtccttccttctc	481	reverse amplicon primer
3223	KIA1526 DOM 1 F	acgtgtctctggtggaaccag	482	forward amplicon pimer
3222	FGFR3 IIIC B NEW R	gcacgtccagcgtgtacgt	483	reverse amplicon primer
3221	FGFR3 IIIC B NEW F	tgcgtcgtggagaacaagttt	484	forward amplicon primer
3220	FGFR3 IIIC A NEW R	acgtccagcgtgtacgtctg	485	reverse amplicon primer
3219	FGFR3 IIIC A NEW F	cgtcgtggagaacaagtttgg	486	forward amplicon primer
3218	HER2 B NEW R	ccacttgatgggcaccttg	487	reverse amplicon primer
3217	HER2 B NEW F	ctgctggacattgacgagaca	488	forward amplicon primer
3216	HER2 A NEW R	ctgtgtacgagccgcacatc	489	reverse amplicon primer
3215	HER2 A NEW F	ctggtgtatgcagattgccaa	490	forward amplicon primer
	VARTUL COMPLETE		491	
3214	R	cagatcgttgcctcccagat		reverse amplicon primer
	VARTUL COMPLETE		492	
3213	F	cgtccctgtcatttctggtca		forward amplicon primer
3212	SITAC18 DOM 1 R	tgccttcttcaccacctgatg	493	reverse amplicon primer
3211	SITAC18 DOM 1 F	gactgtgctgggtggagctc	494	forward amplicon primer
3210	DLG 1 DOM 2 R	cccaggaatatgctgatttcca	495	reverse amplicon primer
3209	DLG 1 DOM 2 F	ggtcttgggtttagcattgctg	496	forward amplicon primer
3208	DLG 1 DOM1 R	tctccaatgtgtgggttgtcc	497	reverse amplicon primer
3207	DLG 1 DOM 1 F	tcagggcttggtttcagcat	498	forward amplicon primer
3206	Ubiquitin R Chamorro	caattgggaatgcaacaactttat	499	reverse amplicon primer
3205	Ubiquitin F Chamorro	cacttggtcctgcgcttga	500	forward amplicon primer
3204	Ubiquitin F	aatcatttgggtcaatatgtaattttca	501	forward amplicon primer
3203	Ubiquitin R	gcggacaatttactagtctaacactga	502	reverse amplicon primer
3202	18S RNA R	gggtcgggagtgggtaattt	503	reverse amplicon primer
3201	18S RNA F	ctaccacatccaaggaaggca	504	forward amplicon primer
3200	PTPL1 dom4 R	cttttggctggatcctgtatgac	505	reverse amplicon primer
3199	PTPL1 dom4 F	tcagagaattggttgttatgttcatg	506	forward amplicon primer
3198	Mupp1 dom 6 R	tccggccatctcgactaatg	507	reverse amplicon primer
3197	Mupp1 dom 6 F	gggatgatcgttcgaagcat	508	forward amplicon primer
3196	Mast 3 com 1 R	agacgtcgctatcacccatgt	509	reverse amplicon primer
3195	Mast 3 dom 1 F	tggcaagaagtacggcttca	510	forward amplicon primer
3194	Kia340 dom 1 R	aacaactttcagacccagcaatg	511	reverse amplicon primer
3193	Kia340 dom 1 F	agaacaaccatgcccaaagact	512	forward amplicon primer

AVC No	Oligo Name	Sequence	SEQ ID NO'	Description
3192	INADL dom 3 R	cctgccctgcatttcgtaa	513	reverse amplicon primer
3191	INADL dom 3 F	cagggttttgccaaccatg	514	forward amplicon primer
3190	PAR 3 dom 3 R	gcccaacagggattctccat	515	reverse amplicon primer
3189	PAR3 dom 3 F	ggcttcgggtgaatgatcaa	516	forward amplicon primer
3188	Pick 1 dom 1 R	cttcgccacctccaccttag	517	reverse amplicon primer
3187	Pick 1 dom 1 F	ggtgtcaatggcaggtcaatc	518	forward amplicon primer
3186	RGS3 dom 1 R	gaatccacggcctggactc	519	reverse amplicon primer
3185	RGS3 dom 1 F	tggcttcaccatctgctgc	520	forward amplicon primer
3184	Sip 1 dom 1 R	cagccttgatcctttgcacc	521	reverse amplicon primer
3183	Sip 1 dom 1 F	gtcaacgtggagggcgag	522	forward amplicon primer
3182	SIP1 dom 2 R	gccgggacttgtcactatgc	523	reverse amplicon primer
3181	SIP 1 dom 2 F	gaaagggacctcagggctatg	524	forward amplicon primer
3180	Tip 1 R	ccaatgctgaaacccaggat	525	reverse amplicon primer
3179	Tip 1 F	aattcacaagctgcgtcaagg	526	forward amplicon primer
3178	AIPC dom 1 F	gggccttggctttagtattgc	527	forward amplicon primer
3177	Mint 3 500 bp R	cagctggcatcgtcttgatatg	528	reverse amplicon primer
3176	Mint 3 500bp F	agctgctcaccgaggcctat	529	forward amplicon primer
3175	Mint 1 dom2 R	cgcatgaggctgcagataatt	530	reverse amplicon primer
3174	Mint 1 dom2 F	ctaccagctcggtttcagcg	531	forward amplicon primer
3173	Mint 1 dom1 R	tctggcaggtggacagagg	532	reverse amplicon primer
3172	Mint 1 dom1 F	cggtgaccagatcatgtccat	533	forward amplicon primer
3171	PTN3 R	acgatttgatccccttcgttc	534	reverse amplicon primer
3170	PTN3 F	agtcacctgcgggacacctg	535	forward amplicon primer
3169	HTRA2 R	gggaaagcttggttctcgaag	536	reverse amplicon primer
3168	HTRA2 F	ctgagtcccagcatccttgc	537	forward amplicon primer
3167	AIPC dom 1 R	ccccatctgtccacgaatg	538	reverse amplicon primer
3166	Mast 2 dom 1 F	acttcttgccagcccttgg	539	forward amplicon primer
3165	Mupp1 dom 3 R	ttggtctccaatttggattcttc	540	reverse amplicon primer
3164	Mupp1 dom 3 F	acaaaaagcagtgccgttga	541	forward amplicon primer
3163	Novel PDZ dom 1 R	cagcacctttacggcgctac	542	reverse amplicon primer
3162	Novel PDZ dom 1 F	aatgggctgagcctggaga	543	forward amplicon primer
3161	MAGI 2 dom 5 F	tgtggacatggagaaaggagc	544	forward amplicon primer
3160	Mast 1 dom 1 R	tgccagacaatgtggtggac	545	reverse amplicon primer
3159	Mast 1 dom 1 F	tgtctacatgggtgacacgga	546	forward amplicon primer
3158	Mast 2 dom 1 R	gctcggtggatgatgatgg	547	reverse amplicon primer
3157	NSP dom 1 R	tcctgagatcacgtctgggaa	548	reverse amplicon primer
3156	NSP dom 1 F	aagccaaagagctgaaggacc	549	forward amplicon primer
3155	Elfin 1 dom 1 R	ccttgcttccaggagtgacc	550	reverse amplicon primer
3154	Elfin 1 dom 1 F	aaaggacttcgagcagcctct	551	forward amplicon primer
3153	EBP50 dom 2 R	tccactaccggatgaactg	552	reverse amplicon primer
3152	EBP50 dom 2 F	caacctgcacagcgacaagt	553	forward amplicon primer
3151	ZO 1 dom 2 R	gcttgccaatcgaagaccat	554	reverse amplicon primer
3150	ZO 1 dom 2 F	acactggtgaaatcccggaa	555	forward amplicon primer
3149	EBP50 dom 1 R	tgtactggcccaacttgcc	556	reverse amplicon primer
3148	EBP50 dom 1 F	agaagggtccgaacggctac	557	forward amplicon primer
3147	APXL dom 1 R	cgcttcctgtctaaaccctga	558	reverse amplicon primer
3146	APXL1 dom 1 F	tgagatcgtcggcatcaatg	559	forward amplicon primer

AVC No	Oligo Name	Sequence	SEQ ID NO'	Description
3145	Grip 2 dom 5 R	gcagttgtccaggcggata	560	reverse amplicon primer
3144	Grip 2 dom 5 F	gagccaggcgacaagctact	561	forward amplicon primer
3143	KIA0382 dom 1 R	atggctgctccatcttctttg	562	reverse amplicon primer
3142	KIA0382 dom 1 F	cggtcagtggagacaatcca	563	forward amplicon primer
3141	Erbin dom 1 R	acaccacctgatatgctaaatcca	564	reverse amplicon primer
3140	Erbin dom 1 F	agtgagggttgaaaaggatcca	565	forward amplicon primer
3139	KIA0316 dom 1 R	tgaccagatcgatgacccg	566	reverse amplicon primer
3138	KIA0316 dom1 F	aatgatgaaccggtcagcg	567	forward amplicon primer
3137	KIA0751(RIM2) dom1 R	aaagccgacctgattcagtca	568	reverse amplicon primer
3136	KIA0751(RIM2) dom 1 F	caatgcttggcttgaaggttg	569	forward amplicon primer
3135	Lim Mystique dom 1R	ccgttgatggccacgattat	570	reverse amplicon primer
3134	Lim Mystique dom 1F	agccaaggacgctgacctc	571	forward amplicon primer
3133	Lim Protein dom1 R	ccttgccgccatcttttaga	572	reverse amplicon primer
3132	Lim Protein dom1 F	cggtaaggatttcaacatgcc	573	forward amplicon primer
3131	MAGI 2 dom 5 R	cctccacgaatgctgaatcc	574	reverse amplicon primer
3116	AIPC As (reverse)	gctgatccatttgggaagatg	575	Amplicon primer for real-time PCR
3115	AIPC S (forward)	gcattcgtggacagatggg	576	Amplicon primer for real-time PCR
3114	HER 1 As (reverse)	cagggattccgtcatatggct	577	Amplicon primer for real-time PCR
3113	HER 1 S (forward)	ccgtttgggagttgatgacc	578	Amplicon primer for real-time PCR
3112	HER 2 As (reverse)	ccacttgatgggcaccttg	579	Amplicon primer for real-time PCR
3111	HER 2 S (forward)	tgctggacattgacgagacag	580	Amplicon primer for real-time PCR
3110	FGFR3C AS (reverse)	cacgtccagcgtgtacgtct	581	Amplicon primer for real-time PCR
3109	FGFR3C S (forward)	ctgcgtcgtggagaacaagtt	582	Amplicon primer for real-time PCR
3108	b-Catenin AS (reverse)	gctgggtatcctgatgtgca	583	Amplicon primer for real-time PCR
3107	b-Catenin S (Forward)	gggtgccattccacgactag	584	Amplicon primer for real-time PCR
3106	MUC-1 AS (reverse)	tgtccagctgcccgtagttc	585	Amplicon primer for real-time PCR
3105	MUC-1 S (forward)	ttgccttggctgtctgtcag	586	Amplicon primer for real-time PCR
3414	RIM2 P7R	tgtggttcaggtttggattctagaa	587	
3413	RIM2 P7F	cacatttgaggaagtgtacaacatcat	588	
3412	RIM2 P6R	tggctccttgcagtagtcttcc	589	
3411	RIM2 P6F	gaccaggtgatgaagtattagaatgg	590	
3410	RIM2 P5R	ccaccaaagtacatcatttcctttt	591	
3409	RIM2 P5F	gtcggactctaacaccaggtctg	592	
3408	RIM2 P4R	tggccaccaaagtacatcatttc	593	
3407	RIM2 P4F	ctctaacaccaggtctgagagacaaa	594	
3406	RIM2 P3R	ttggttccatttgggttcca	595	
3405	RIM2 P3F	ttccagacagaagtgataaaaacaagag	596	
3404	RIM2 P2R	tgcattgttcagtgtttgtcca	597	
3403	RIM2 P2F	ccaccaaatatcttacaaaatgagctt	598	
3402	RIM2 P1R	tccagatcagcatttgccaa	599	
3393	RIM2 P1F	acggcatgagagaaggcatag	600	